

*results of* **BLAST****BLASTN 2.2.6 [Apr-09-2003]**

RID: 1064960959-20664-530139.BLASTQ3

Query=

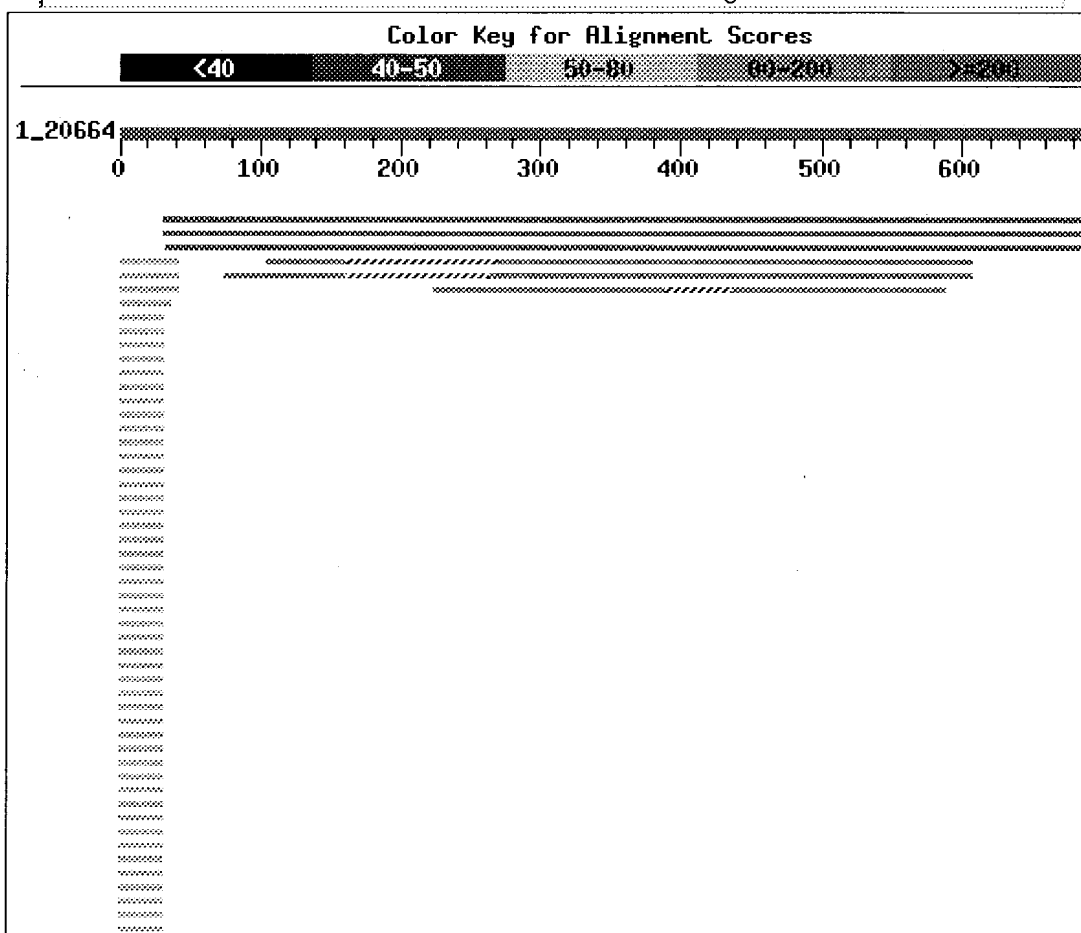
(689 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)

1,931,681 sequences; 9,156,315,655 total letters

Taxonomy reports**Distribution of 106 Blast Hits on the Query Sequence**

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value

gi 505280 emb X59040.1 CBDPEXC3	Clostridium botulinum D pha...	1261	0.0
gi 296786 emb X59039.1 CBCPEXC3	Clostridium botulinum C pha...	1261	0.0
gi 14907 emb X51464.1 CBDPE3	Clostridium botulinum D Phage ...	1257	0.0
gi 144736 gb M74038.1 CLOC3ADP	C.botulinum C3 ADP-ribosyltr...	184	1e-43
gi 404820 dbj D17555.1 CLOADPRC3	Clostridium botulinum type...	172	5e-40
gi 1212874 emb X87215.1 CLC3GENE	C.limosum C3 gene	100	6e-18
gi 33149672 gb AY330212.1 	Cloning vector pT3, complete seq...	68	2e-08
gi 595779 gb U13871.1 XXU13871	pT7T3D cloning vector, compl...	68	2e-08
gi 595774 gb U13869.1 XXU13869	pT7T318U cloning vector, com...	68	2e-08
gi 1149706 emb X86491.1 CPSPFOOA	C.perfringens spoOA gene	66	9e-08
gi 31335236 gb AY292466.1 	BAC cloning vector pBACVM4, comp...	64	3e-07
gi 30424554 gb AY182782.1 	Shuttle vector pSK5640, complete...	64	3e-07
gi 30424549 gb AY182781.1 	Shuttle vector pSK5632, complete...	64	3e-07
gi 29838547 gb AY265466.1 	Shuttle vector pAM2770, complete...	64	3e-07
gi 29825787 gb AY263154.1 	Cloning vector pAM2600, complete...	64	3e-07
gi 29415162 gb AY150268.1 	CRIM plasmid pSK67, complete seq...	64	3e-07
gi 29373934 gb AY219701.1 	Cloning vector pAZ1, complete se...	64	3e-07
gi 22595311 gb AF405697.1 	Reporter vector pALH122, complet...	64	3e-07
gi 28207668 gb AY187276.1 	Shuttle vector pBSV2, complete s...	64	3e-07
gi 21952452 gb AF524829.1 	P-element cloning system vector ...	64	3e-07
gi 21952450 gb AF524828.1 	P-element cloning system vector ...	64	3e-07
gi 21780275 gb AF521666.1 	Cloning vector pLOI2065 complete...	64	3e-07
gi 25141017 gb AC116033.2 	Zea mays genomic clone ZM15C05 ...	64	3e-07
gi 22074797 gb AY112734.1 	Broad host range vector pMLS7, c...	64	3e-07
gi 22074788 gb AY112733.1 	Broad host range vector pMLBAD, ...	64	3e-07
gi 5824688 emb AL110477.1 CEY113G7B	Caenorhabditis elegans ...	64	3e-07
gi 34556140 emb BX005348.8 	Zebrafish DNA sequence from clo...	64	3e-07
gi 33457134 emb AJ560658.1 SSC560658	Sus scrofa partial mRN...	64	3e-07
gi 4567137 gb AF134471.1 	Homo sapiens chromosome 10 clone ...	64	3e-07
gi 21617574 gb AF519766.1 	Cloning vector pMAK705, complete...	64	3e-07
gi 21328627 gb AE008921.1 	Uncultured proteobacterium clone...	64	3e-07
gi 11559661 gb AF294978.1 	Cloning vector pC1300intC, compl...	64	3e-07
gi 11559659 gb AF294977.1 	Cloning vector pC1300intB, compl...	64	3e-07
gi 11559657 gb AF294976.1 	Cloning vector pC1300intA, compl...	64	3e-07
gi 20141090 gb L09137.2 SYNPUC19CV	Cloning vector pUC19c, c...	64	3e-07
gi 20455693 gb AC110750.4 	Homo sapiens chromosome 17, clon...	64	3e-07
gi 5419758 emb AJ246004.1 HSA246004	Homo sapiens RET gene, ...	64	3e-07
gi 18766962 gb AF480833.1 	Cloning vector pNOT218 beta-lact...	64	3e-07
gi 18654300 gb L47837.1 SYNKIL199P	Cloning vector pKIL199 c...	64	3e-07
gi 18654298 gb L47836.1 SYNKIL198P	Cloning vector pKIL198 c...	64	3e-07
gi 14794622 gb AF327719.1 AF327719	Cloning vector pCM130, c...	64	3e-07
gi 14794608 gb AF327717.1 AF327717	Cloning vector pCM160, c...	64	3e-07
gi 14794600 gb AF327716.1 AF327716	Cloning vector pCM80, co...	64	3e-07
gi 14794593 gb AF327715.1 AF327715	Cloning vector pCM66, co...	64	3e-07
gi 14794585 gb AF327714.1 AF327714	Cloning vector pCM62, co...	64	3e-07
gi 14794547 gb AF327711.1 AF327711	Cloning vector pDN19, co...	64	3e-07
gi 18041969 gb AF337031.1 AF337031	Aphidius ervi clone 110 ...	64	3e-07
gi 18041957 gb AF337016.1 AF337016	Aphidius ervi clone 34 m...	64	3e-07
gi 18041950 gb AF337003.1 AF337003	Aphidius ervi clone 13R ...	64	3e-07
gi 18041946 gb AF336997.1 AF336997	Aphidius ervi clone 107 ...	64	3e-07
gi 18041941 gb AF336992.1 AF336992	Aphidius ervi clone 47 m...	64	3e-07
gi 18041939 gb AF336990.1 AF336990	Aphidius ervi clone 4 mi...	64	3e-07
gi 13161000 gb AF325903.1 AF325903	Cloning vector pFH2191, ...	64	3e-07
gi 13540351 gb AF354046.1 AF354046	Binary vector pCAMBIA-13...	64	3e-07
gi 13540346 gb AF354045.1 AF354045	Binary vector pCAMBIA-13...	64	3e-07
gi 13345295 gb AF323603.1 AF323603	Cloning vector pPOP, com...	64	3e-07
gi 8308058 gb AF261959.1 AF261959	Anourosorex squamipes clo...	64	3e-07
gi 9294791 gb AF178451.1 AF178451	Integration vector pCD11P...	64	3e-07
gi 8927566 gb AF276982.1 AF276982	Integrative vector pNLE1,...	64	3e-07

gi 8650401 gb AF216802.1 AF216802	Shuttle vector pDL278, co...	64	3e-07
gi 8272485 gb AF219942.1 AF219942	Shuttle vector pPha-T1 co...	64	3e-07
gi 7715975 gb AF203972.1 AF203972	Shuttle vector pBA comple...	64	3e-07
gi 7705080 gb AC068564.1 AC068564	Filobasidiella neoformans...	64	3e-07
gi 5689998 emb AJ131112.1 SSC131112	Sus scrofa MHC class I ...	64	3e-07
gi 28300623 emb AL953891.10	Zebrafish DNA sequence from cl...	64	3e-07
gi 7638149 gb AF234316.1 AF234316	Binary vector pCAMBIA-230...	64	3e-07
gi 7638145 gb AF234315.1 AF234315	Binary vector pCAMBIA-230...	64	3e-07
gi 7638140 gb AF234314.1 AF234314	Binary vector pCAMBIA-220...	64	3e-07
gi 7638136 gb AF234313.1 AF234313	Binary vector pCAMBIA-220...	64	3e-07
gi 7638083 gb AF234300.1 AF234300	Binary vector pCAMBIA-130...	64	3e-07
gi 7638078 gb AF234299.1 AF234299	Binary vector pCAMBIA-130...	64	3e-07
gi 7638073 gb AF234298.1 AF234298	Binary vector pCAMBIA-130...	64	3e-07
gi 7638068 gb AF234297.1 AF234297	Binary vector pCAMBIA-130...	64	3e-07
gi 7638064 gb AF234296.1 AF234296	Binary vector pCAMBIA-130...	64	3e-07
gi 7638049 gb AF234293.1 AF234293	Binary vector pCAMBIA-120...	64	3e-07
gi 7638045 gb AF234292.1 AF234292	Binary vector pCAMBIA-120...	64	3e-07
gi 7415878 dbj AB038146.1	Cloning vector pGFPTA DNA, compl...	64	3e-07
gi 27531019 dbj AB082961.1	Cloning vector pMG171 DNA, comp...	64	3e-07
gi 27531016 dbj AB082960.1	Cloning vector pMG170 DNA, comp...	64	3e-07
gi 15553040 dbj AB055652.1	Thermosensitive suicide vector ...	64	3e-07
gi 15553035 dbj AB055651.1	Thermosensitive suicide vector ...	64	3e-07
gi 15553030 dbj AB055650.1	Thermosensitive suicide vector ...	64	3e-07
gi 8250423 emb AJ271043.1 MBA271043	Marine bacterium S5 par...	64	3e-07
gi 4884786 gb AF128862.1 AF128862	Cloning vector pHIND2.2, ...	64	3e-07
gi 4731624 gb AF134573.1 AF134573	Cloning vector p34S-Sm3, ...	64	3e-07
gi 4731621 gb AF134572.1 AF134572	Cloning vector p34S-Sm2, ...	64	3e-07
gi 3907623 gb AF102233.1 AF102233	Transposon delivery vecto...	64	3e-07
gi 3136321 gb AF064067.1 AF064067	Expression vector pYZ81N,...	64	3e-07
gi 3136317 gb AF064066.1 AF064066	Expression vector pYZ41N,...	64	3e-07
gi 29164976 gb AY219695.1	Shuttle vector pBHT18mob2, compl...	64	3e-07
gi 29164973 gb AY219694.1	Shuttle vector pBHK18mob2, compl...	64	3e-07
gi 29164970 gb AY219693.1	Shuttle vector pBHC18mob2, compl...	64	3e-07
gi 29164967 gb AY219692.1	Shuttle vector pBHT18, complete ...	64	3e-07
gi 29164964 gb AY219691.1	Shuttle vector pBHK18, complete ...	64	3e-07
gi 29164961 gb AY219690.1	Shuttle vector pBHC18, complete ...	64	3e-07
gi 29164958 gb AY219689.1	Expression vector pXT99A, comple...	64	3e-07
gi 29164955 gb AY219688.1	Expression vector pXS99A, comple...	64	3e-07
gi 29164951 gb AY219687.1	Expression vector pXK99CAT, comp...	64	3e-07
gi 4827116 dbj AP000150.1	Homo sapiens genomic DNA, chromo...	64	3e-07
gi 6468567 emb AJ131034.1 HSA131034	Homo sapiens otase gene...	58	2e-05

Alignments

Get selected sequences	Select all	Deselect all
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☒ >gi|505280|emb|X59040.1|CBDPEXC3 Clostridium botulinum D phage gene for exoenzym
Length = 1979

Score = 1261 bits (636), Expect = 0.0
Identities = 654/659 (99%), Gaps = 1/659 (0%)
Strand = Plus / Plus

Query: 32 atgcttattccattaatcaaaa-ggcttattcaaatacttaccaggaggtttactaatattg 90
|||||

Sbjct: 823 atgcttattccattaatcaaaaggcttattcaaatacttaccaggagtttactaatattg 882

Query: 91 atcaagcaaaagcttggggtaatgctcagtataaaaagtatggactaagcaaatcagaaa 150
 |||

Sbjct: 883 atcaagcaaaagcttggggtaatgctcagtataaaaagtatggactaagcaaatcagaaa 942

Query: 151 aagaagctatagtatcatataactaaaagcgctagtgaataaatggaaagctaagacaaa 210
 |||

Sbjct: 943 aagaagctatagtatcatataactaaaagcgctagtgaataaatggaaagctaagacaaa 1002

Query: 211 ataaggaggattatcaatggatttccttcaaatttaataaaacaagttgaacttttagata 270
 |||

Sbjct: 1003 ataaggaggattatcaatggatttccttcaaatttaataaaacaagttgaacttttagata 1062

Query: 271 aatcttttaataaaaatgaagaccctgaaaatattatgttatttagaggcgacgaccctg 330
 |||

Sbjct: 1063 aatcttttaataaaaatgaagaccctgaaaatattatgttatttagaggcgacgaccctg 1122

Query: 331 cttatttaggaacagaatttcaaaacactcttcttaattcaaattgtacaattaataaaa 390
 |||

Sbjct: 1123 cttatttaggaacagaatttcaaaacactcttcttaattcaaattgtacaattaataaaa 1182

Query: 391 cggcttttgaaaaggctaaagctaagtttttaataaaagatagacttgaatatggatata 450
 |||

Sbjct: 1183 cggcttttgaaaaggctaaagctaagtttttaataaaagatagacttgaatatggatata 1242

Query: 451 ttagtacttcattaatgaatgtttctcaatttgcaggaagaccaattattacanaattta 510
 |||

Sbjct: 1243 ttagtacttcattaatgaatgtttctcaatttgcaggaagaccaattattacaaaattta 1302

Query: 511 aagtagcaaaaggctcaaaggcaggatatattgaccctattagtgttttcagggacaac 570
 |||


Sbjct: 1303 aagtagcaaaaggctcaaaggcaggatatattgaccctattagtgttttcagggacaac 1362

Query: 571 ttgaaatgttgcttccttagacatagtagtacttatcatatagacgatatgagattgtcttctg 630
 |||

Sbjct: 1363 ttgaaatgttgcttccttagacatagtagtacttatcatatagacgatatgagattgtcttctg 1422

Query: 631 atggtaacaaataataattacagcaacaatgatgggcacagctatcaatcctaaataa 689
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Sbjct: 1423 atggtaacaaataataattacagcaacaatgatgggcacagctatcaatcctaaataa 1481

 >gi|296786|emb|X59039.1|CBCPEXC3 Clostridium botulinum C phage gene for exoenzym
 Length = 1977

Score = 1261 bits (636), Expect = 0.0
 Identities = 654/659 (99%), Gaps = 1/659 (0%)
 Strand = Plus / Plus

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Query: 32   atgcttattccattaatcaaaa-ggcttattcaaatacttaccaggagtttactaatattg 90
          |||
Sbjct: 821  atgcttattccattaatcaaaaaggcttattcaaatacttaccaggagtttactaatattg 880

Query: 91   atcaagcaaaaagcttggggtaatgctcagtataaaaagtatggactaagcaaatcagaaa 150
          |||
Sbjct: 881  atcaagcaaaaagcttggggtaatgctcagtataaaaagtatggactaagcaaatcagaaa 940

Query: 151  aagaagctatagtatcatataactaaaagcgctagtgaataaatggaaagctaagacaaa 210
          |||
Sbjct: 941  aagaagctatagtatcatataactaaaagcgctagtgaataaatggaaagctaagacaaa 1000

Query: 211  ataaggaggattatcaatggatttccttcaaatttaataaaaacaagttgaacttttagata 270
          |||
Sbjct: 1001 ataaggaggattatcaatggatttccttcaaatttaataaaaacaagttgaacttttagata 1060

Query: 271  aatcttttaataaaaatgaagacccttgaaaatattatggtatttagaggcgacgaccctg 330
          |||
Sbjct: 1061 aatcttttaataaaaatgaagacccttgaaaatattatggtatttagaggcgacgaccctg 1120

Query: 331  cttatttaggaacagaatttcaaaacactcttcttaattcaaattggtacaattaataaaa 390
          |||
Sbjct: 1121 cttatttaggaacagaatttcaaaacactcttcttaattcaaattggtacaattaataaaa 1180

Query: 391  cggcttttgaaaaggctaaaagctaagtttttaataaagatagacttgaatatggatata 450
          |||
Sbjct: 1181 cggcttttgaaaaggctaaaagctaagtttttaataaagatagacttgaatatggatata 1240


Query: 451  ttagtacttcattaatgaatgtttctcaatttgcaggaagaccaattattacanaattta 510
          |||
Sbjct: 1241 ttagtacttcattaatgaatgtttctcaatttgcaggaagaccaattattacanaattta 1300

Query: 511  aagtagcaaaaaggctcaaaggcaggatatattgaccctattagtgccttttcagggacaac 570
          |||
Sbjct: 1301 aagtagcaaaaaggctcaaaggcaggatatattgaccctattagtgccttttcagggacaac 1360

Query: 571  ttgaaatggttgcttcctagacatagtagtacttatcatatagacgatatgagattgtcttctg 630
          |||
Sbjct: 1361 ttgaaatggttgcttcctagacatagtagtacttatcatatagacgatatgagattgtcttctg 1420

Query: 631  atggtaaacaaataataattacagcaacaatgatgggcacagctatcaatcctaaataa 689
          |||
Sbjct: 1421 atggtaaacaaataataattacagcaacaatgatgggcacagctatcaatcctaaataa 1479

```

 >gi|14907|emb:X51464.1|CBDPE3
Length = 780

Clostridium botulinum D Phage C3 gene for exoenzym

Score = 1257 bits (634), Expect = 0.0
 Identities = 652/657 (99%), Gaps = 1/657 (0%)
 Strand = Plus / Plus

Query: 34 gcttattccattaatcaaaa-ggcttattcaaatacttaccaggaggtttactaatattgat 92
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
 Sbjct: 1 gcttattccattaatcaaaaaggcttattcaaatacttaccaggaggtttactaatattgat 60

Query: 93 caagcaaaaagcttggggtaatgctcagtataaaaagtatggactaagcaaatcagaaaaa 152
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
 Sbjct: 61 caagcaaaaagcttggggtaatgctcagtataaaaagtatggactaagcaaatcagaaaaa 120

Query: 153 gaagctatagtatcatataactaaaagcgctagtgaataaaatggaaagctaagacaaaaat 212
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
 Sbjct: 121 gaagctatagtatcatataactaaaagcgctagtgaataaaatggaaagctaagacaaaaat 180

Query: 213 aagggagttatcaatggatttccttcaaatttaataaaaacaagttgaacttttagataaa 272
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
 Sbjct: 181 aagggagttatcaatggatttccttcaaatttaataaaaacaagttgaacttttagataaa 240

Query: 273 tcttttaataaaaatgaagacccctgaaaatattatgttatttagaggcgacgaccctgct 332
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
 Sbjct: 241 tcttttaataaaaatgaagacccctgaaaatattatgttatttagaggcgacgaccctgct 300

Query: 333 tatttaggaacagaatttcaaaacactcttcttaattcaaattgtacaattaataaaaacg 392
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
 Sbjct: 301 tatttaggaacagaatttcaaaacactcttcttaattcaaattgtacaattaataaaaacg 360

Query: 393 gcttttgaaaaggctaaagctaagtttttaataaaagatagacttgaatatggatatatt 452
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
 Sbjct: 361 gcttttgaaaaggctaaagctaagtttttaataaaagatagacttgaatatggatatatt 420

Query: 453 agtacttcattaatgaatgtttctcaatttgcaggaagaccaattattacanaatttaaa 512
 |||||||||||||||||| |||||||||||||||||||||| ||||||||
 Sbjct: 421 agtacttcattaatgaatgtttctcaatttgcaggaagaccaattattacaaaatttaaa 480

Query: 513 gtagcaaaaaggctcaaaggcaggatatattgaccctattagtgccttttcagggacaactt 572
 |||||||||||||||||| |||||||||||||||||| ||||||||
 Sbjct: 481 gtagcaaaaaggctcaaaggcaggatatattgaccctattagtgccttttcagggacaactt 540

Query: 573 gaaatgttgcttcctagacatagttacttatcatatagacgatatgagattgtcttctgat 632
 |||||||||||||||||| |||||||||||||||||||||| ||||||||
 Sbjct: 541 gaaatgttgcttcctagacatagttacttatcatatagacgatatgagattgtcttctgat 600

Query: 633 ggtaaacaataataattacagcaacaatgatgggcacagctatcaatcctaaataa 689
 |||||||||||||||||| |||||||||||||||||| ||||||||
 Sbjct: 601 ggtaaacaataataattacagcaacaatgatgggcacagctatcaatcctaaataa 657

Score = 184 bits (93), Expect = 1e-43
Identities = 277/338 (81%), Gaps = 3/338 (0%)
Strand = Plus / Plus

```
Query: 571      ttgaaatgttgcttcctagacatagtactttatcatata 608
          ||||| ||||| ||||| ||| || ||| |||||
Sbjct: 1069     ttgaagtgttgcttcctagaaataaatagttattatata 1106
```

Score = 58.0 bits (29), Expect = 2e-05
Identities = 50/57 (87%)
Strand = Plus / Plus

Query: 105 tggggtaatgctcagtataaaaaagtatggactaagcaaatcagaaaaagaagctata 161
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 606 tggggaaatgctcaatatataaaaaatatggcctaagcaaacctgaacaagaagctata 662

```
>gi|404820|db|D17555.1|CLOADPRC3 Clostridium botulinum type D gene for ADP-ribo
complete cds
Length = 1712
```

Score = 172 bits (87), Expect = 5e-40
Identities = 280/344 (81%), Gaps = 3/344 (0%)
Strand = Plus / Plus

Query: 265 tagataaatcttttaataaaatgaagaccctgaaaatattatgttatttagaggcgacg 324
 ||||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
 Sbjct: 764 tagatcaatcttttagtaagatgaagatgcctcaaaatattattcttttagagggtgatg 823

Query: 325 accctgcttatttaggaacagaatttcaaaacactcttcttaattcaaattggtacaatta 384
 ||||| ||||| ||||| ||||| ||| ||||| ||| ||||| |||
 Sbjct: 824 accctgcttatttaggtccagaatttcaagataaaattcttaataaagatggaacaatta 883

Query: 385 ataaaacggcttttgaaaaggctaaagctaagtttttaataaagatagacttgaatatg 444
 ||| | | ||||| | | ||||| || ||||| ||||| |||||
 Sbjct: 884 atagagatgttttgaacaagttaaagcgaaatttttaaaaaaagatagaacagaatatg 943

Query: 445 gatataattagtagtcttcattaatgaatgtttctcaatttgcaggaagaccaattattacan 504
 ||||| ||||| ||||| ||||| ||| | ||||| ||||| ||||| |||||
 Sbjct: 944 gatataattagtagtcttcattaatgagtg---cgcaatttggaggaagaccaattgttacta 1000


Query: 505 aatttaaagtagcaaaaggctcaaaggcaggatatattgaccctattagtgcttttcagg 564
 ||||| ||||| | || || ||||| | || ||||| ||||| ||||| |||||
 Sbjct: 1001 aatttaaagtaactaatggatcaaaaggagggtatatagaccctattagctatttccag 1060

Query: 565 gacaacttgaaatgttgcttcctagacatagtagtattatcatata 608
 ||||| ||||| ||||| ||||| ||| || ||||| |||||
 Sbjct: 1061 gacaacttgaaatgttgcttcctagaaataatagttattatata 1104

Score = 61.9 bits (31), Expect = 1e-06
 Identities = 73/87 (83%)
 Strand = Plus / Plus

Query: 75 gagtttactaatattgatcaagcaaaagcttggggaatgctcagtataaaaagtatgga 134
 ||||| ||||| ||||| ||||| ||| ||||| ||||| ||||| |||||
 Sbjct: 574 gagtttactaatgttgagggaagccaaaaaatggggaatgctcaatataaaaaaatatggc 633

Query: 135 ctaagcaaatacagaaaaagaagctata 161
 ||||| ||| ||||| |||||
 Sbjct: 634 ctaagcaaacctgaacaagaagctata 660

 >gi|1212674|emb|Z87215.1|CLC3GENE C.limosum C3 gene
 Length = 1022

Score = 99.6 bits (50), Expect = 6e-18
 Identities = 127/153 (83%)
 Strand = Plus / Plus

Query: 438 gaatatggatatattagtagtcttcattaatgaatgtttctcaatttgcaggaagaccaatt 497
 ||||| ||||| ||||| ||||| ||| ||||| ||||| ||||| |||||
 Sbjct: 673 gaatatggatatattagtagtctttagtaaatgggttcagcatttgcaggttagaccaatt 732

☐ >gi|595774|gb|U13869.1|XXU13869 pT7T318U cloning vector, complete sequence
Length = 2883

Score = 67.9 bits (34), Expect = 2e-08
Identities = 41/42 (97%), Gaps = 1/42 (2%)
Strand = Plus / Minus

Query: 1 ggatcctctagagtcgacctgcaggcatgcaatgcttattcc 42
|||||
Sbjct: 230 ggatcctctagagtcgacctgcaggcatgcaa-gcttattcc 190

☐ >gi|1149706|emb|X86491.1|CPSP00A C.perfringens spoOA gene
Length = 350

Score = 65.9 bits (33), Expect = 9e-08
Identities = 36/37 (97%)
Strand = Plus / Plus

Query: 1 ggatcctctagagtcgacctgcaggcatgcaatgctt 37
|||||
Sbjct: 275 ggatcctctagagtcgacctgcaggcatgcaaggctt 311

☐ >gi|31335236|gb|AY292466.1| BAC cloning vector pBACVM4, complete sequence
Length = 9077

Score = 63.9 bits (32), Expect = 3e-07
Identities = 32/32 (100%)
Strand = Plus / Plus

Query: 1 ggatcctctagagtcgacctgcaggcatgcaa 32
|||||
Sbjct: 1813 ggatcctctagagtcgacctgcaggcatgcaa 1844

☐ >gi|30424554|gb|AY182782.1| Shuttle vector pSK5640, complete sequence
Length = 6152

Score = 63.9 bits (32), Expect = 3e-07
Identities = 32/32 (100%)
Strand = Plus / Minus

Query: 1 ggatcctctagagtcgacctgcaggcatgcaa 32
|||||
Sbjct: 36 ggatcctctagagtcgacctgcaggcatgcaa 5